

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
OLIVE, DAVID M.
- (ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF PATHOGENS
- (iii) NUMBER OF SEQUENCES: 160
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MEDLEN & CARROLL
 - (B) STREET: 220 MONTGOMERY STREET, SUITE 2200
 - (C) CITY: SAN FRANCISCO
 - (D) STATE: CALIFORNIA
 - (E) COUNTRY: UNITED STATES OF AMERICA
 - (F) ZIP: 94104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: CARROLL, PETER G.
 - (B) REGISTRATION NUMBER: 32,837
 - (C) REFERENCE/DOCKET NUMBER: FORS-01756
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 705-8410
 - (B) TELEFAX: (415) 397-8338

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGGGGGA TGCTGCCCCT CTTTGAGCCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC	60
CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG GGGGGAGCCG	120
GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTCAAGGA GGACGGGGAC	180
GCGGTGATCG TGGTCTTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC CTACGGGGGG	240
TACAAGGCGG GCCGGGCCCC CACGCCGGAG GACTTTCCCC GGCAACTCGC CCTCATCAAG	300

GAGCTGGTGG ACCTCCTGGG GCTGGCGCGC CTCGAGGTCC CGGGCTACGA GGCGGACGAC	360
GTCCTGGCCA GCCTGGCCAA GAAGGCGGAA AAGGAGGGCT ACGAGGTCCG CATCCTCACC	420
GGCGACAAAG ACCTTTACCA GCTCCTTTCC GACCGCATCC ACGTCCTCCA CCCCAGGGG	480
TACCTCATCA CCCC GGCTG GCTTTGGGAA AAGTACGGCC TGAGGCCCGA CCAGTGGGCC	540
GACTACCGGG CCCTGACCGG GGACGAGTCC GACAACCTTC CCGGGGTCAA GGGCATCGGG	600
GAGAAGACGG CGAGGAAGCT TCTGGAGGAG TGGGGGAGCC TGGAAGCCCT CCTCAAGAAC	660
CTGGACCGGC TGAAGCCCGC CATCCGGGAG AAGATCCTGG CCCACATGGA CGATCTGAAG	720
CTCTCCTGGG ACCTGGCCAA GGTGCGCACC GACCTGCCCC TGGAGGTGGA CTTCGCCAAA	780
AGGCGGGAGC CCGACCGGGA GAGGCTTAGG GCCTTTCTGG AGAGGCTTGA GTTTGGCAGC	840
CTCCTCCACG AGTTCGGCCT TCTGGAAAGC CCAAGGCCCC TGGAGGAGGC CCCCTGGCCC	900
CCGCCGGAAG GGGCCTTCGT GGGCTTTGTG CTTTCCCGCA AGGAGCCCAT GTGGGCCGAT	960
CTTCTGGCCC TGGCCGCCGC CAGGGGGGGC CGGGTCCACC GGGCCCCCGA GCCTTATAAA	1020
GCCCTCAGGG ACCTGAAGGA GGCGCGGGGG CTCTCGCCA AAGACCTGAG CGTTCTGGCC	1080
CTGAGGGAAG GCCTTGCCCT CCCGCCCGGC GACGACCCCA TGCTCCTCGC CTACCTCCTG	1140
GACCCTTCCA ACACCACCC CGAGGGGGTG GCCCGGCGCT ACGGCGGGGA GTGGACGGAG	1200
GAGGCGGGGG AGCGGGCCGC CCTTTCCGAG AGGCTCTTCG CCAACCTGTG GGGGAGGCTT	1260
GAGGGGGAGG AGAGGCTCCT TTGGCTTTAC CGGGAGGTGG AGAGGCCCCCT TTCCGCTGTC	1320
CTGGCCCACA TGGAGGCCAC GGGGGTGCGC CTGGACGTGG CCTATCTCAG GGCCTTGTCE	1380
CTGGAGGTGG CCGAGGAGAT CGCCCGCCTC GAGGCCGAGG TCTTCCGCCT GGCCGGCCAC	1440
CCCTTCAACC TCAACTCCCG GGACCAGCTG GAAAGGGTCC TCTTTGACGA GCTAGGGCTT	1500
CCCGCCATCG GCAAGACGGA GAAGACCGGC AAGCGCTCCA CCAGCGCCGC CGTCCTGGAG	1560
GCCCTCCGCG AGGCCCACCC CATCGTGGAG AAGATCCTGC AGTACCGGGA GCTCACCAAG	1620
CTGAAGAGCA CCTACATTGA CCCCTTGCCG GACCTCATCC ACCCCAGGAC GGGCCGCCTC	1680
CACACCCGCT TCAACCAGAC GGCCACGGCC ACGGGCAGGC TAAGTAGCTC CGATCCCAAC	1740
CTCCAGAACA TCCCCGTCCG CACCCCGCTT GGGCAGAGGA TCCGCCGGGC CTTTCATCGCC	1800
GAGGAGGGGT GGCTATTGGT GGCCCTGGAC TATAGCCAGA TAGAGCTCAG GGTGCTGGCC	1860
CACCTCTCCG GCGACGAGAA CCTGATCCGG GTCTTCCAGG AGGGGCGGGA CATCCACAG	1920
GAGACCGCCA GCTGGATGTT CGGCGTCCCC CGGGAGGCCG TGGACCCCTT GATGCGCCGG	1980
GCGGCCAAGA CCATCAACTT CGGGGTCCCTC TACGGCATGT CGGCCCACCG CCTCTCCCAG	2040
GAGCTAGCCA TCCCTTACGA GGAGGCCAG GCCTTCATTG AGCGCTACTT TCAGAGCTTC	2100
CCCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG GGGGTACGTG	2160

GAGACCCTCT TCGGCCGCGG CCGCTACGTG CCAGACCTAG AGGCCCGGGT GAAGAGCGTG	2220
CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC ATGCCCCTCC AGGGCACCGC CGCCGACCTC	2280
ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGG AAATGGGGGC CAGGATGCTC	2340
CTTCAGGTCC ACGACGAGCT GGTCTCTGAG GCCCCAAAAG AGAGGGCGGA GGCCGTGGCC	2400
CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCCT GGAGGTGGAG	2460
GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC	2506

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGCGATGC TTCCCCTCTT TGAGCCCAA AAA GGCCGCGTGC TCCTGGTGGA CGGCCACCAC	60
CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGG CGAACCCGTT	120
CAGGCGGTCT ACGGCTTCGC CAAAAGCCTC CTCAAGGCCC TGAAGGAGGA CGGGGACGTG	180
GTGGTGGTGG TCTTTGACGC CAAGGCCCCC TCCTTCCGCC ACGAGGCCTA CGAGGCCTAC	240
AAGGCGGGCC GGGCCCCCACC CCCGGAGGAC TTTCCCCGGC AGCTGGCCCT CATCAAGGAG	300
TTGGTGGACC TCCTAGGCCT TGTGCGGCTG GAGGTTCCCC GCTTTGAGGC GGACGACGTG	360
CTGGCCACCC TGGCCAAGCG GCGGAAAAG GAGGGGTACG AGGTGCGCAT CCTCACTGCC	420
GACCGCGACC TCTACCAGCT CCTTTCCGAG CGCATCGCCA TCCTCCACCC TGAGGGGTAC	480
CTGATCACCC CGGCGTGGCT TTACGAGAAG TACGGCCTGC GCCCGGAGCA GTGGGTGGAC	540
TACCGGGCCC TGGCGGGGA CCCCTCGGAT AACATCCCCG GGGTGAAGGG CATCGGGGAG	600
AAGACCGCCC AGAGGCTCAT CCGCGAGTGG GGGAGCCTGG AAAACCTCTT CCAGCACCTG	660
GACCAGGTGA AGCCCTCCTT GCGGGAGAAG CTCCAGGCGG GCATGGAGGC CCTGGCCCTT	720
TCCCGGAAGC TTTCCAGGT GCACACTGAC CTGCCCCTGG AGGTGGACTT CGGGAGGCGC	780
CGCACACCCA ACCTGGAGGG TCTGCGGGCT TTTTGGAGC GGTGGAGTT TGGAAGCCTC	840
CTCCACGAGT TCGGCCTCCT GGAGGGGCGG AAGGCGGCAG AGGAGGCCCC CTGGCCCCCT	900
CCGGAAGGGG CTTTTTTGGG CTTTTCTTTT TCCCGTCCCG AGCCCATGTG GGCCGAGCTT	960
CTGGCCCTGG CTGGGGCGTG GGAGGGGCGC CTCCATCGGG CACAAGACCC CCTTAGGGGC	1020
CTGAGGGACC TTAAGGGGGT GCGGGGAATC CTGGCCAAGG ACCTGGCGGT TTTGGCCCTG	1080
CGGGAGGGCC TGGACCTCTT CCCAGAGGAC GACCCCATGC TCCTGGCCTA CCTTCTGGAC	1140

CCCTCCAACA CCACCCCTGA GGGGGTGGCC CGGCGTTACG GGGGGGAGTG GACGGAGGAT	1200
GCGGGGGAGA GGGCCCTCCT GGCCGAGCGC CTCTTCCAGA CCCTAAAGGA GCGCCTTAAG	1260
GGAGAAGAAC GCCTGCTTTG GCTTTACGAG GAGGTGGAGA AGCCGCTTTC CCGGGTGTG	1320
GCCCGGATGG AGGCCACGGG GGTCCGGCTG GACGTGGCCT ACCTCCAGGC CCTCTCCCTG	1380
GAGGTGGAGG CGGAGGTGCG CCAGCTGGAG GAGGAGGTCT TCCGCCTGGC CGGCCACCCC	1440
TTCAACCTCA ACTCCCGCGA CCAGCTGGAG CGGGTGTCTT TTGACGAGCT GGGCCTGCCT	1500
GCCATCGGCA AGACGGAGAA GACGGGGAAA CGCTCCACCA GCGCTGCCGT GCTGGAGGCC	1560
CTGCGAGAGG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGGGAGCT CACCAAGCTC	1620
AAGAACACCT ACATAGACCC CTGCCCCGCC CTGGTCCACC CCAAGACCGG CCGGCTCCAC	1680
ACCCGCTTCA ACCAGACGGC CACCGCCACG GGCAGGCTTT CCAGCTCCGA CCCCAACCTG	1740
CAGAACATCC CCGTGCGCAC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCGAG	1800
GAGGGCTGGG TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCCAC	1860
CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG	1920
ACCGCCAGCT GGATGTTCCG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG	1980
GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG	2040
CTTTCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC	2100
AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGGG GTATGTGGAG	2160
ACCCTCTTCG GCCGCCGGCG CTATGTGCCG GACCTCAACG CCCGGGTGAA GAGCGTGCGE	2220
GAGGCGGCGG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCGC CGACCTCATG	2280
AAGCTGGCCA TGGTGCGGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG	2340
CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCAAGGACC GGGCGGAGAG GGTAGCCGCT	2400
TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG	2460
GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG	2496

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGAGGCGA TGCTTCCGCT CTTTGAACCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC	60
CACCTGGCCT ACCGCACCTT CTTCGCCCTG AAGGGCTCA CCACGAGCCG GGGCGAACCG	120

GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGTAC	180
AAGGCCGTCT TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGAG	240
GCCTACAAGG CGGGGAGGGC CCCGACCCCC GAGGACTTCC CCCGGCAGCT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGTTTACC CGCCTCGAGG TCCCCGGCTA CGAGGCGGAC	360
GACGTTCTCG CCACCCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC	420
ACCGCCGACC GCGACCTCTA CCAACTCGTC TCCGACCGCG TCGCCGTCCT CCACCCCGAG	480
GGCCACCTCA TCACCCCGGA GTGGCTTTGG GAGAAGTACG GCCTCAGGCC GGAGCAGTGG	540
GTGGACTTCC GCGCCCTCGT GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CCGCCCTCAA GCTCCTCAAG GAGTGGGGAA GCCTGGAAAA CCTCCTCAAG	660
AACCTGGACC GGGTAAAGCC AGAAAACGTC CGGGAGAAGA TCAAGGCCCA CCTGGAAGAC	720
CTCAGGCTCT CTTGGAGCT CTCCCGGGTG CGCACCGACC TCCCCCTGGA GGTGGACCTC	780
GCCCAGGGGC GGGAGCCCGA CCGGGAGGGG CTTAGGGCCT TCCTGGAGAG GCTGGAGTTC	840
GGCAGCCTCC TCCACGAGTT CGGCCTCCTG GAGGCCCCCG CCCCCCTGGA GGAGGCCCCC	900
TGGCCCCCGC CGGAAGGGGC CTTCGTGGGC TTCGTCCTCT CCCGCCCCGA GCCCATGTGG	960
GCGGAGCTTA AAGCCCTGGC CGCCTGCAGG GACGGCCGGG TGCACCGGGC AGCAGACCCC	1020
TTGGCGGGGC TAAAGGACCT CAAGGAGGTC CGGGGCCTCC TCGCCAAGGA CCTCGCCGTC	1080
TTGGCCTCGA GGGAGGGGCT AGACCTCGTG CCCGGGGACG ACCCATGCT CCTCGCCTAC	1140
CTCCTGGACC CCTCCAACAC CACCCCCGAG GGGGTGGCGC GGCGCTACGG GGGGGAGTGG	1200
ACGGAGGACG CCGCCCACCG GGCCCTCCTC TCGGAGAGGC TCCATCGGAA CTCCTTAAG	1260
CGCCTCGAGG GGGAGGAGAA GCTCCTTTGG CTCTACCACG AGGTGGAAAA GCCCCTCTCC	1320
CGGGTCCTGG CCCACATGGA GGCCACCGGG GTACGGCTGG ACGTGGCCTA CCTTCAGGCC	1380
CTTTCCCTGG AGCTTGCGGA GGAGATCCGC CGCCTCGAGG AGGAGGTCTT CCGCTTGGCG	1440
GGCCACCCCT TCAACCTCAA CTCCCGGGAC CAGCTGGAAA GGGTGCTCTT TGACGAGCTT	1500
AGGCTTCCCG CCTTGGGGAA GACGCAAAAG ACAGGCAAGC GCTCCACCAG CGCCGCGGTG	1560
CTGGAGGCCC TACGGGAGGC CCACCCATC GTGGAGAAGA TCCTCCAGCA CCGGGAGCTC	1620
ACCAAGCTCA AGAACACCTA CGTGGACCCC CTCCAAGCC TCGTCCACCC GAGGACGGGC	1680
CGCCTCCACA CCCGCTTCAA CCAGACGGCC ACGGCCACGG GGAGGCTTAG TAGCTCCGAC	1740
CCCAACCTGC AGAACATCCC CGTCCGCACC CCCTTGGGCC AGAGGATCCG CCGGGCCTTC	1800
GTGGCCGAGG CGGGTTGGGC GTTGGTGGCC CTGGACTATA GCCAGATAGA GCTCCGCGTC	1860
CTCGCCCAAC TCTCCGGGGA CGAAAACCTG ATCAGGGTCT TCCAGGAGGG GAAGGACATC	1920
CACACCCAGA CCGCAAGCTG GATGTTCCGC GTCCCCCGG AGGCCGTGGA CCCCCTGATG	1980

CGCCGGGCGG CCAAGACGGT GAACTTCGGC GTCCTCTACG GCATGTCCGC CCATAGGCTC 2040
 TCCCAGGAGC TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGGC TACTTCCAAA 2100
 GCTTCCCCAA GGTGCGGGCC TGGATAGAAA AGACCCTGGA GGAGGGGAGG AAGCGGGGCT 2160
 ACGTGGAAC CCTCTTCGGA AGAAGGCGCT ACGTGCCCGA CCTCAACGCC CGGGTGAAGA 2220
 GCGTCAGGGA GGCCGCGGAG CGCATGGCCT TCAACATGCC CGTCCAGGGC ACCGCCGCCG 2280
 ACCTCATGAA GCTCGCCATG GTGAAGCTCT TCCCCGCCT CCGGGAGATG GGGGCCCGCA 2340
 TGCTCCTCCA GGTCCACGAC GAGCTCTCTC TGGAGGCCCC CCAAGCGCGG GCCGAGGAGG 2400
 TGGCGGCTTT GGCCAAGGAG GCCATGGAGA AGGCCTATCC CCTCGCCGTG CCCCTGGAGG 2460
 TGGAGGTGGG GATGGGGGAG GACTGGCTTT CCGCCAAGGG TTAG 2504

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Arg	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	1	5	10	15
Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	Gly	20	25	30	
Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	35	40	45	
Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	Val	50	55	60	
Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	Gly	65	70	75	80
Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	85	90	95	
Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	Glu	100	105	110	
Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	Lys	115	120	125	
Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	Asp	130	135	140	
Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	Gly	145	150	155	160
Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	165	170	175	

Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn
180 185 190

Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu
195 200 205

Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu
210 215 220

Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys
225 230 235 240

Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val
245 250 255

Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe
260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
275 280 285

Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
290 295 300

Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp
305 310 315 320

Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro
325 330 335

Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu
340 345 350

Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro
355 360 365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
370 375 380

Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
385 390 395 400

Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu
405 410 415

Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu
420 425 430

Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly
435 440 445

Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala
450 455 460

Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His
465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
485 490 495

Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
500 505 510

09940925-082801

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
515 520 525

Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr
530 535 540

Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu
545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
565 570 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
580 585 590

Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala
595 600 605

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
610 615 620

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
625 630 635 640

Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro
645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
660 665 670

Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
675 680 685

Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
690 695 700

Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
705 710 715 720

Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg
725 730 735

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
740 745 750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
755 760 765

Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His
770 775 780

Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala
785 790 795 800

Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
805 810 815

Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu
820 825 830

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 831 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1           5           10           15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
          20           25           30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
        35           40           45

Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Val Val Val Val Val
50           55           60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala Tyr
65           70           75           80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
          85           90           95

Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Val Arg Leu Glu Val
        100          105          110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Arg Ala
        115          120          125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
        130          135          140

Tyr Gln Leu Leu Ser Glu Arg Ile Ala Ile Leu His Pro Glu Gly Tyr
        145          150          155          160

Leu Ile Thr Pro Ala Trp Leu Tyr Glu Lys Tyr Gly Leu Arg Pro Glu
          165          170          175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
          180          185          190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Gln Arg Leu Ile Arg
        195          200          205

Glu Trp Gly Ser Leu Glu Asn Leu Phe Gln His Leu Asp Gln Val Lys
        210          215          220

Pro Ser Leu Arg Glu Lys Leu Gln Ala Gly Met Glu Ala Leu Ala Leu
        225          230          235          240

Ser Arg Lys Leu Ser Gln Val His Thr Asp Leu Pro Leu Glu Val Asp
          245          250          255

Phe Gly Arg Arg Arg Thr Pro Asn Leu Glu Gly Leu Arg Ala Phe Leu
          260          265          270

Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu

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109140925-082801

275	280	285
Gly Pro Lys Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala		
290	295	300
Phe Leu Gly Phe Ser Phe Ser Arg Pro Glu Pro Met Trp Ala Glu Leu		
305	310	315
Leu Ala Leu Ala Gly Ala Trp Glu Gly Arg Leu His Arg Ala Gln Asp		
	325	330
Pro Leu Arg Gly Leu Arg Asp Leu Lys Gly Val Arg Gly Ile Leu Ala		
	340	345
Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Phe Pro		
	355	360
Glu Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr		
	370	375
Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp		
385	390	395
Ala Gly Glu Arg Ala Leu Leu Ala Glu Arg Leu Phe Gln Thr Leu Lys		
	405	410
Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu Val		
	420	425
Glu Lys Pro Leu Ser Arg Val Leu Ala Arg Met Glu Ala Thr Gly Val		
	435	440
Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Glu Ala		
	450	455
Glu Val Arg Gln Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro		
465	470	475
Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu		
	485	490
Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser		
	500	505
Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val		
	515	520
Asp Arg Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr		
	530	535
Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Gly Arg Leu His		
545	550	555
Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser		
	565	570
Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg		
	580	585
Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Val Leu Val Val Leu		
	595	600

Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
610 615 620

Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Gln
625 630 635 640

Thr Ala Ser Trp Met Phe Gly Val Ser Pro Glu Gly Val Asp Pro Leu
645 650 655

Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met
660 665 670

Ser Ala His Arg Leu Ser Gly Glu Leu Ser Ile Pro Tyr Glu Glu Ala
675 680 685

Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg Ala
690 695 700

Trp Ile Glu Gly Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu
705 710 715 720

Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val
725 730 735

Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
740 745 750

Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Arg Leu Phe
755 760 765

Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His Asp
770 775 780

Glu Leu Val Leu Glu Ala Pro Lys Asp Arg Ala Glu Arg Val Ala Ala
785 790 795 800

Leu Ala Lys Glu Val Met Glu Gly Val Trp Pro Leu Gln Val Pro Leu
805 810 815

Glu Val Glu Val Gly Leu Gly Glu Asp Trp Leu Ser Ala Lys Glu
820 825 830

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
1 5 10 15

Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly
20 25 30

Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
35 40 45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg
130 135 140

Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu
145 150 155 160

Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu
195 200 205

Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg
210 215 220

Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp
225 230 235 240

Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu
245 250 255

Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg
260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
275 280 285

Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro
290 295 300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
305 310 315 320

Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg
325 330 335

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
340 345 350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
355 360 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
370 375 380

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Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	385	390	395	400
Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	His	Arg	405	410	415	
Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	Leu	Tyr	420	425	430	
His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	435	440	445	
Thr	Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	450	455	460	
Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	465	470	475	480
Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	485	490	495	
Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Lys	Thr	Gly	500	505	510	
Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	515	520	525	
Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	530	535	540	
Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly	545	550	555	560
Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	565	570	575	
Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	580	585	590	
Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu	595	600	605	
Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	610	615	620	
Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	625	630	635	640
His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	645	650	655	
Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	660	665	670	
Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	675	680	685	
Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	690	695	700	
Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	705	710	715	720

AGCCTCCTCC ACGAGTTCGG CCTCCTGGAG GGCCCCAAGG CCCTGGAGGA GGCCCCCTGG	900
CCCCCGCCGG AAGGGGCCTT CGTGGGCTTT GTCCTTTCCC GCCCCGAGCC CATGTGGGCC	960
GAGCTTCTGG CCCTGGCCGC CGCCAGGGAG GGCCGGGTCC ACCGGGCACC AGACCCCTTT	1020
ANGGGCCTNA GGGACCTNAA GGAGGTGCGG GGNCTCCTCG CCAAGGACCT GGCCGTTTTG	1080
GCCCTGAGGG AGGGCCTNGA CCTCNTGCCC GGGGACGACC CCATGCTCCT CGCCTACCTC	1140
CTGGACCCCT CCAACACCAC CCCCAGGGG GTGGCCCGGC GCTACGGGGG GGAGTGGACG	1200
GAGGANGCGG GGGAGCGGC CCTCCTNTCC GAGAGGCTCT TCCNGAACCT NNNGCAGCGC	1260
CTTGAGGGGG AGGAGAGGCT CCTTTGGCTT TACCAGGAGG TGGAGAAGCC CCTTTCCCGG	1320
GTCCTGGCCC ACATGGAGGC CACGGGGGTN CGGCTGGACG TGGCCTACCT CCAGGCCCTN	1380
TCCCTGGAGG TGGCGGAGGA GATCCGCCGC CTCGAGGAGG AGGTCTTCCG CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAAGGG TGCTCTTTGA CGAGCTNGGG	1500
CTTCCCGCCA TCGGCAAGAC GGAGAAGACN GGCAAGCGCT CCACCAGCGC CGCCGTGCTG	1560
GAGGCCCTNC GNGAGGCCCA CCCCATCGTG GAGAAGATCC TGCAGTACCG GGAGCTCACC	1620
AAGCTCAAGA ACACCTACAT NGACCCCTG CCNGNCCTCG TCCACCCAG GACGGGCCGC	1680
CTCCACACCC GCTTCAACCA GACGGCCACG GCCACGGGCA GGCTTAGTAG CTCCGACCCC	1740
AACCTGCAGA ACATCCCCGT CCGCACCCCN CTGGGCCAGA GGATCCGCCG GGCTTTCGTG	1800
GCCGAGGAGG GNTGGGTGTT GGTGGCCCTG GACTATAGCC AGATAGAGCT CCGGGTCCTG	1860
GCCCACCTCT CCGGGGACGA GAACCTGATC CGGGTCTTCC AGGAGGGGAG GGACATCCAC	1920
ACCCAGACCG CCAGCTGGAT GTTCGGCGTC CCCCCGAGG CCGTGGACCC CCTGATGCGC	1980
CGGGCGGCCA AGACCATCAA CTTCGGGGTC CTCTACGGCA TGTCCGCCCA CCGCCTCTCC	2040
CAGGAGCTTG CCATCCCCTA CGAGGAGGCG GTGGCCTTCA TTGAGCGCTA CTTCCAGAGC	2100
TTCCCCAAGG TGCGGGCCTG GATTGAGAAG ACCCTGGAGG AGGGCAGGAG GCGGGGTAC	2160
GTGGAGACCC TCTTCGGCCG CCGGCGCTAC GTGCCCGACC TCAACGCCCG GGTGAAGAGC	2220
GTGCGGGAGG CGGCGGAGCG CATGGCCTTC AACATGCCCG TCCAGGGCAC CGCCGCCGAC	2280
CTCATGAAGC TGGCCATGGT GAAGCTCTC CCCC GGCTNC AGGAAATGGG GGCCAGGATG	2340
CTCCTNCAGG TCCACGACGA GCTGGTCCTC GAGGCCCCCA AAGAGCGGGC GGAGGNGGTG	2400
GCCGCTTTGG CCAAGGAGGT CATGGAGGGG GTCTATCCCC TGGCCGTGCC CCTGGAGGTG	2460
GAGGTGGGGA TGGGGGAGGA CTGGCTCTCC GCCAAGGAGT AG	2502

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Xaa Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
1 5 10 15
Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly
20 25 30
Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
35 40 45
Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Xaa Val
50 55 60
Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala
65 70 75 80
Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
85 90 95
Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Xaa Arg Leu Glu
100 105 110
Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys
115 120 125
Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp
130 135 140
Leu Tyr Gln Leu Leu Ser Asp Arg Ile Ala Val Leu His Pro Glu Gly
145 150 155 160
Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
165 170 175
Glu Gln Trp Val Asp Tyr Arg Ala Leu Xaa Gly Asp Pro Ser Asp Asn
180 185 190
Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Xaa Lys Leu Leu
195 200 205
Xaa Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val
210 215 220
Lys Pro Xaa Xaa Arg Glu Lys Ile Xaa Ala His Met Glu Asp Leu Xaa
225 230 235 240
Leu Ser Xaa Xaa Leu Ser Xaa Val Arg Thr Asp Leu Pro Leu Glu Val
245 250 255
Asp Phe Ala Xaa Arg Arg Glu Pro Asp Arg Glu Gly Leu Arg Ala Phe
260 265 270
Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
275 280 285
Glu Xaa Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
290 295 300

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Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
305 310 315 320

Leu Leu Ala Leu Ala Ala Ala Arg Xaa Gly Arg Val His Arg Ala Xaa
325 330 335

Asp Pro Leu Xaa Gly Leu Arg Asp Leu Lys Glu Val Arg Gly Leu Leu
340 345 350

Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Xaa
355 360 365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
370 375 380

Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
385 390 395 400

Asp Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Xaa Asn Leu
405 410 415

Xaa Xaa Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Xaa Glu
420 425 430

Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
435 440 445

Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Ala
450 455 460

Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
485 490 495

Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
515 520 525

Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr
530 535 540

Tyr Ile Asp Pro Leu Pro Xaa Leu Val His Pro Arg Thr Gly Arg Leu
545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
565 570 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
580 585 590

Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Xaa Leu Val Ala
595 600 605

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
610 615 620

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
625 630 635 640

Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
660 665 670

Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
675 680 685

Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
690 695 700

Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
705 710 715 720

Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
725 730 735

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
740 745 750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
755 760 765

Phe Pro Arg Leu Xaa Glu Met Gly Ala Arg Met Leu Leu Gln Val His
770 775 780

Asp Glu Leu Val Leu Glu Ala Pro Lys Xaa Arg Ala Glu Xaa Val Ala
785 790 795 800

Ala Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
805 810 815

Leu Glu Val Glu Val Gly Xaa Gly Glu Asp Trp Leu Ser Ala Lys Glu
820 825 830

Xaa

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1647 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC	60
CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG	120
CCGGTGCAGG CGGTCTACGG CTTCCGCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG	180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG	240
GGGTACAAGG CCGGCCCGGC CCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC	360

GACGTCCTGG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC	420
ACCGCCGACA AAGACCTTTA CCAGCTCCTT TCCGACCGCA TCCACGTCCT CCACCCCGAG	480
GGGTACCTCA TCACCCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG	540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCACAT GGACGATCTG	720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTCGCC	780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTTGGC	840
AGCCTCCTCC ACAGATTCCG CTTTCTGGAA AGCCCCAAGG CCCTGGAGGA GGCCCCCTGG	900
CCCCCGCCGG AAGGGGCCTT CGTGGGCTTT GTGCTTTCCC GCAAGGAGCC CATGTGGGCC	960
GATCTTCTGG CCCTGGCCGC CGCCAGGGGG GGCCGGGTCC ACCGGGCCCC CGAGCCTTAT	1020
AAAGCCCTCA GGGACCTGAA GGAGGCGCGG GGGCTTCTCG CCAAAGACCT GAGCGTTCTG	1080
GCCCTGAGGG AAGGCCCTGG CCTCCCGCCC GCGGACGACC CCATGCTCCT CGCCTACCTC	1140
CTGGACCCTT CCAACACCAC CCCCAGGGGG GTGGCCCGGC GCTACGGCGG GGAGTGGACG	1200
GAGGAGGCGG GGGAGCGGGC CGCCCTTTCC GAGAGGCTCT TCGCCAACCT GTGGGGGAGG	1260
CTTGAGGGGG AGGAGAGGCT CTTTGGCTT TACCGGGAGG TGGAGAGGCC CTTTCCGCT	1320
GTCCTGGCCC ACATGGAGGC CACGGGGGTG CGCCTGGACG TGGCCTATCT CAGGGCCTTG	1380
TCCCTGGAGG TGGCCGGGGA GATCGCCCGC CTCGAGGCCG AGGTCTTCCG CCTGGCCGGE	1440
CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAGGG TCCTCTTTGA CGAGCTAGGG	1500
CTTCCCGCCA TCGGCAAGAC GGAGAAGACC GGCAAGCGCT CCACCAGCGC CGCCGTCCTG	1560
GAGGCCCTCC GCGAGGCCCA CCCCATCGTG GAGAAGATCC TGCAGGCATG CAAGCTTGGC	1620
ACTGGCCGTC GTTTTACAAC GTCGTGA	1647

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2088 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC	60
CACCACCTGG CCTACCGCAC CTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG	120
CCGGTGCAGG CGGTCTACGG CTTCGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG	180

GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG	240
GGGTACAAGG CGGGCCGGGC CCCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC	360
GACGTCTCTG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC	420
ACCGCCGACA AAGACCTTTA CCAGCTCCTT TCCGACCGCA TCCACGTCCT CCACCCCGAG	480
GGGTACCTCA TCACCCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG	540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCACAT GGACGATCTG	720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGAATTGCCC	780
AAAAGGCGGG AGCCCCACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTTGGC	840
AGCCTCCTCC ACGAGTTCGG CCTTCTGGAA AGCCCCAAGG CCCTGGAGGA GGCCCCCTGG	900
CCCCCGCCGG AAGGGGCCTT CGTGGGCTTT GTGCTTTCCC GCAAGGAGCC CATGTGGGCC	960
GATCTTCTGG CCCTGGCCGC CGCCAGGGGG GGCCGGGTCC ACCGGGCCCC CGAGCCTTAT	1020
AAAGCCCTCA GGGACCTGAA GGAGGCGCGG GGGCTTCTCG CCAAAGACCT GAGCGTTCTG	1080
GCCCTGAGGG AAGGCCTTGG CCTCCCGCCC GCGACGACC CCATGCTCCT CGCCTACCTC	1140
CTGGACCCTT CCAACACCAC CCCCAGGGGG GTGGCCCGGC GCTACGGCGG GGAGTGGACG	1200
GAGGAGGCGG GGGAGCGGGC CGCCCTTTCC GAGAGGCTCT TCGCCAACCT GTGGGGGAGG	1260
CTTGAGGGGG AGGAGAGGCT CCTTTGGCTT TACCGGGAGG TGGAGAGGCC CCTTTCCGCT	1320
GTCCTGGCCC ACATGGAGGC CACGGGGGTG CGCCTGGACG TGGCCTATCT CAGGGCCTTG	1380
TCCCTGGAGG TGGCCGGGGA GATCGCCCGC CTCGAGGCCG AGGTCTTCCG CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAGGG TCCTCTTTGA CGAGCTAGGG	1500
CTTCCCGCCA TCGGCAAGAC GGAGAAGACC GGCAAGCGCT CCACCAGCGC CGCCGTCCTG	1560
GAGGCCCTCC GCGAGGCCCC CCCCATCGTG GAGAAGATCC TGCAGTACCG GGAGCTCACC	1620
AAGCTGAAGA GCACCTACAT TGACCCCTTG CCGGACCTCA TCCACCCAG GACGGGCCGC	1680
CTCCACACCC GCTTCAACCA GACGGCCACG GCCACGGGCA GGCTAAGTAG CTCCGATCCC	1740
AACCTCCAGA ACATCCCCGT CCGCACCCCG CTTGGGCAGA GGATCCGCCG GGCCTTCATC	1800
GCCGAGGAGG GGTGGCTATT GGTGGCCCTG GACTATAGCC AGATAGAGCT CAGGGTGCTG	1860
GCCCACCTCT CCGGCGACGA GAACCTGATC CGGGTCTTCC AGGAGGGGCG GGACATCCAC	1920
ACGGAGACCG CCAGCTGGAT GTTCGGCGTC CCCCAGGAGG CCGTGGACCC CCTGATGCGC	1980
CGGGCGGCCA AGACCATCAA CTTCGGGGTC CTCTACGGCA TGTCGGCCCA CCGCCTCTCC	2040

CAGGAGCTAG CTAGCCATCC CTTACGAGGA GGCCAGGCC TTCATTGA

2088

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 962 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC 60
CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG 120
CCGGTGCAGG CGGTCTACGG CTTCCGCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG 180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG 240
GGGTACAAGG CGGGCCGGGC CCCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC 300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC 360
GACGTCCTGG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC 420
ACCGCCGACA AAGACCTTTA CCAGCTTCTT TCCGACCGCA TCCACGTCCT CCACCCCGAG 480
GGGTACCTCA TCACCCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG 540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC 600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG 660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCACAT GGACGATCTG 720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTCGCC 780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTTGGC 840
AGCCTCCTCC ACGAGTTCGG CTTTCTGGAA AGCCCCAAGT CATGGAGGGG GTGTATCCCC 900
TGGCCGTGCC CCTGGAGGTG GAGGTGGGGA TAGGGGAGGA CTGGCTCTCC GCCAAGGAGT 960
GA 962

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1600 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGGAATTCG GGGATGCTGC CCCTCTTGA GCCCAAGGGC CGGGTCCTCC TGGTGGACGG 60

CCACCACCTG GCCTACCGCA CCTTCCACGC CCTGAAGGGC CTCACCACCA GCCGGGGGGA	120
GCCGGTGCAG GCGGTCTACG GCTTCGCCAA GAGCCTCCTC AAGGCCCTCA AGGAGGACGG	180
GGACGCGGTG ATCGTGGTCT TTGACGCCAA GGCCCCCTCC TTCCGCCACG AGGCCTACGG	240
GGGTACAAG GCGGGCCGGG CCCCCACGCC GGAGGACTTT CCCC GGCAAC TCGCCCTCAT	300
CAAGGAGCTG GTGGACCTCC TGGGGCTGGC GCGCCTCGAG GTCCCGGGCT ACAGGGCGGA	360
CGACGTCCTG GCCAGCCTGG CCAAGAAGGC GGAAAAGGAG GGCTACGAGG TCCGCATCCT	420
CACCGCCGAC AAAGACCTTT ACCAGCTCCT TTCCGACCGC ATCCACGTCC TCCACCCCGA	480
GGGTACCTC ATCACCCCGG CCTGGCTTTG GGAAAAGTAC GGCCTGAGGC CCGACCAAGT	540
GGCCGACTAC CGGGCCCTGA CCGGGGACGA GTCCGACAAC CTTCCCGGGG TCAAGGGCAT	600
CGGGGAGAAG ACGGCGAGGA AGCTTCTGGA GGAGTGGGGG AGCCTGGAAG CCCTCCTCAA	660
GAACCTGGAC CGGCTGAAGC CCGCCATCCG GGAGAAGATC CTGGCCCACA TGGACGATCT	720
GAAGCTCTCC TGGGACCTGG CCAAGGTGCG CACCGACCTG CCCCTGGAGG TGGACTTCGC	780
CAAAAGGCGG GAGCCCGACC GGGAGAGGCT TAGGGCCTTT CTGGAGAGGC TTGAGTTTGG	840
CAGCCTCTC CACGAGTTG GCCTTCTGGA AAGCCCCAAG ATCCGCCGGG CCTTCATCGC	900
CGAGGAGGGG TGGCTATTGG TGGCCCTGGA CTATAGCCAG ATAGAGCTCA GGGTGCTGGC	960
CCACCTCTCC GCGGACGAGA ACCTGATCCG GGTCTTCCAG GAGGGGCGGG ACATCCACAC	1020
GGAGACCGCC AGCTGGATGT TCGGCGTCCC CCGGAGAGCC GTGGACCCCC TGATGCGCCG	1080
GGCGGCCAAG ACCATCAACT TCGGGGTCCT CTACGGCATG TCGGCCACC GCCTCTCCCA	1140
GGAGCTAGCC ATCCCTTACG AGGAGGCCCA GGCCTTCATT GAGCGCTACT TTCAGAGCTT	1200
CCCCAAGGTG CGGGCCTGGA TTGAGAAGAC CCTGGAGGAG GGCAGGAGGC GGGGGTACGT	1260
GGAGACCTC TTCGGCCGCC GCCGCTACGT GCCAGACCTA GAGGCCCGGG TGAAGAGCGT	1320
GCGGGAGGCG GCCGAGCGCA TGGCCTTCAA CATGCCCGTC CGGGGCACCG CCGCCGACCT	1380
CATGAAGCTG GCTATGGTGA AGCTCTTCCC CAGGCTGGAG GAAATGGGGG CCAGGATGCT	1440
CCTTCAGGTC CACGACGAGC TGGTCCTCGA GGCCCCAAAA GAGAGGGCGG AGGCCGTGGC	1500
CCGGCTGGCC AAGGAGGTCA TGGAGGGGGT GTATCCCCTG GCCGTGCCCC TGGAGGTGGA	1560
GGTGGGGATA GGGGAGGACT GGCTCTCCGC CAAGGAGTGA	1600

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACGAATTCG GGGATGCTGC CCCTCTTTGA GCCCAA

36

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTGAGATCTA TCACTCCTTG GCGGAGAGCC AGTC

34

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAATACGACT CACTATAGGG AGACCGGAAT TCGAGCTCGC CCGGGCGAGC TCGAATTCCG

60

TGTATTCTAT AGTGTACCT AAATCGAATT C

91

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAATACGACT CACTATAGGG

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGATT TAGGTGACAC TATAGAA

27

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTAATCATGG TCATAGCTGG TAGCTTGCTA C

31

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGATCCTCTA GAGTCGACCT GCAGGCATGC CTACCTTGGT AG

42

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATCCTCTA GAGTCGACCT GCAGGCATGC

30

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC

60

CACCACCTGG CCTACCGCAC CTTCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG

120

CCGGTGCAGG CGGTCTACGG CTCGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG

180

GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG

240

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108280"52604660

GGGTACAAGG	CGGGCCGGGC	CCCCACGCCG	GAGGACTTTC	CCCGGCAACT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGCTGGCG	CGCCTCGAGG	TCCCGGGCTA	CGAGGCGGAC	360
GACGTCCTGG	CCAGCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GCTACGAGGT	CCGCATCCTC	420
ACCGCCGACA	AAGACCTTTA	CCAGCTCCTT	TCCGACCGCA	TCCACGTCCT	CCACCCCGAG	480
GGGTACCTCA	TCACCCCGGC	CTGGCTTTGG	GAAAAGTACG	GCCTGAGGCC	CGACCAGTGG	540
GCCGACTACC	GGGCCCTGAC	CGGGGACGAG	TCCGACAACC	TTCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CGGCGAGGAA	GCTTCTGGAG	GAGTGGGGGA	GCCTGGAAGC	CCTCCTCAAG	660
AACCTGGACC	GGCTGAAGCC	CGCCATCCGG	GAGAAGATCC	TGGCCACAT	GGACGATCTG	720
AAGCTCTCCT	GGGACCTGGC	CAAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGGCGGG	AGCCCGACCG	GGAGAGGCTT	AGGGCCTTTC	TGGAGAGGCT	TGAGTTTGGC	840
AGCCTCCTCC	ACGAGTTCGG	CCTTCTGGAA	AGCCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
CCCCCGCCGG	AAGGGGCCTT	CGTGGGCTTT	GTGCTTTCCC	GCAAGGAGCC	CATGTGGGCC	960
GATCTTCTGG	CCCTGGCCGC	CGCCAGGGGG	GGCCGGGTCC	ACCGGGCCCC	CGAGCCTTAT	1020
AAAGCCCTCA	GGGACCTGAA	GGAGGCGCGG	GGGCTTCTCG	CCAAAGACCT	GAGCGTTCTG	1080
GCCCTGAGGG	AAGGCCTTGG	CCTCCCGCCC	GGCGACGACC	CCATGCTCCT	CGCCTACCTC	1140
CTGGACCCTT	CCAACACCAC	CCCCGAGGGG	GTGGCCCGGC	GCTACGGCGG	GGAGTGGACG	1200
GAGGAGGCGG	GGGAGCGGGC	CGCCCTTTCC	GAGAGGCTCT	TCGCCAACCT	GTGGGGGAGG	1260
CTTGAGGGGG	AGGAGAGGCT	CCTTTGGCTT	TACCGGGAGG	TGGAGAGGCC	CCTTTCCGCT	1320
GTCCTGGCCC	ACATGGAGGC	CACGGGGGTG	CGCCTGGACG	TGGCCTATCT	CAGGGCCTTG	1380
TCCCTGGAGG	TGGCCGGGGA	GATCGCCCGC	CTCGAGGCCG	AGGTCTTCCG	CCTGGCCGGC	1440
CACCCCTTCA	ACCTCAACTC	CCGGGACCAG	CTGGAAAGGG	TCCTCTTTGA	CGAGCTAGGG	1500
CTTCCCGCCA	TCGGCAAGAC	GGAGAAGACC	GGCAAGCGCT	CCACCAGCGC	CGCCGTCCTG	1560
GAGGCCCTCC	GCGAGGCCCA	CCCCATCGTG	GAGAAGATCC	TGCAGTACCG	GGAGCTCACC	1620
AAGCTGAAGA	GCACCTACAT	TGACCCCTTG	CCGACCTCA	TCCACCCAG	GACGGGCCGC	1680
CTCCACACCC	GCTTCAACCA	GACGGCCACG	GCCACGGGCA	GGCTAAGTAG	CTCCGATCCC	1740
AACCTCCAGA	ACATCCCCGT	CCGCACCCCG	CTTGGGCAGA	GGATCCGCCG	GGCCTTCATC	1800
GCCGAGGAGG	GGTGGCTATT	GGTGGCCCTG	GACTATAGCC	AGATAGAGCT	CAGGGTGCTG	1860
GCCCACCTCT	CCGGCGACGA	GAACCTGATC	CGGGTCTTCC	AGGAGGGGCG	GGACATCCAC	1920
ACGGAGACCG	CCAGCTGGAT	GTTCGGCGTC	CCCCGGGAGG	CCGTGGACCC	CCTGATGCGC	1980
CGGGCGGCCA	AGACCATCAA	CTTCGGGGTC	CTCTACGGCA	TGTCGGCCCA	CCGCCTCTCC	2040
CAGGAGCTAG	CCATCCCTTA	CGAGGAGGCC	CAGGCCTTCA	TTGAGCGCTA	CTTTCAGAGC	2100

TTCCCCAAGG TCGGGCCTG GATTGAGAAG ACCCTGGAGG AGGGCAGGAG GCGGGGGTAC 2160
GTGGAGACCC TCTTCGGCCG CGCCGCTAC GTGCCAGACC TAGAGGCCCG GGTGAAGAGC 2220
GTGCGGGAGG CGGCCGAGCG CATGGCCTTC AACATGCCCG TCCGGGGCAC CGCCGCCGAC 2280
CTCATGAAGC TGGCTATGGT GAAGCTCTTC CCCAGGCTGG AGGAAATGGG GGCCAGGATG 2340
CTCCTTCAGG TCCACGACGA GCTGGTCCTC GAGGCCCCAA AAGAGAGGGC GGAGGCCGTG 2400
GCCCCGCTGG CCAAGGAGGT CATGGAGGGG GTGTATCCCC TGGCCGTGCC CCTGGAGGTG 2460
GAGGTGGGGA TAGGGGAGGA CTGGCTCTCC GCCAAGGAGT GA 2502

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATTTAGGTG AACTATAG 19

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGGACGAACA AGCGAGACAG CGACACAGGT ACCACATGGT ACAAGAGGCA AGAGAGACGA 60

CACAGCAGAA AC 72

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTTTCTGCTG TGTCGTCTCT CTTGCCTCTT GTACCATGTG GTACCTGTGT CGCTGTCTCG 60

CTTGTTTCGTC 70

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GACGAACAAG CGAGACAGCG

20

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTTTCTGCTG TGTCGTCTCT CTTG

24

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCTCTTGCTAC CATGTGGTAC CTGTGTCGCT GTCTCGCTTG TTCGTC

46

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACACAGGTAC CACATGGTAC AAGAGGCAAG AGAGACGACA CAGCAGAAAC

50

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTCCGATCA ATTCGGGGAT GCTGCCCCCTC 60
TTTGAGCCCA AGGGCCGGGT CCTCCTGGTG GACGGCCACC ACCTGGCCTA CCGCACCTTC 120
CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCGGT CTACGGCTTC 180
GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTTGAC 240
GCCAAGGCCC CCTCCTTCCG CCACGAGGCC TACGGGGGGT ACAAGGCGGG CCGGGCCCCC 300
ACGCCGGAGG ACTTTCCCCG GCAACTCGCC CTCATCAAGG AGCTGGTGGA CCTCCTGGGG 360
CTGGCGCGCC TCGAGGTCCC GGGCTACGAG GCGGACGACG TCCTGGCCAG CCTGGCCAAG 420
AAGGCGGAAA AGGAGGGCTA CGAGGTCCGC ATCCTCACCG CCGACAAAGA CCTTTACCAG 480
CTTCTTTCCG ACCGCATCCA CGTCCTCCAC CCCGAGGGGT ACCTCATCAC CCCGGCCTGG 540
CTTTGGGAAA AGTACGGCCT GAGGCCCGAC CAGTGGGCGG ACTACCGGGC CCTGACCGGG 600
GACGAGTCCG ACAACCTTCC CGGGGTCAAG GGCATCGGGG AGAAGACGGC GAGGAAGCTT 660
CTGGAGGAGT GGGGGAGCCT GGAAGCCCTC CTCAAGAACC TGGACCGGCT GAAGCCC GCC 720
ATCCGGGAGA AGATCCTGGC CCACATGGAC GATCTGAAGC TCTCCTGGGA CCTGGCCAAG 780
GTGCGCACCG ACCTGCCCCT GGAGGTGGAC TTCGCCAAA GCGGGGAGCC CGACCGGGAG 840
AGGCTTAGGG CCTTTCTGGA GAGGCTTGAG TTTGGCAGCC TCCTCCACGA GTTCGGCCTT 900
CTGGAAAGCC CCAAGTCATG GAGGGGGTGT ATCCCCTGGC CGTGCCCTG GAGGTGGAGG 960
TGGGGATAG 969

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTCGGATCA ATTCGGGGAT GCTGCCCCCTC	60
TTTGAGCCCA AGGGCCGGGT CCTCCTGGTG GACGGCCACC ACCTGGCCTA CCGCACCTTC	120
CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCGGT CTACGGCTTC	180
GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTTGAC	240
GCCAAGGCCC CCTCCTTCCG CCACGAGGCC TACGGGGGGT ACAAGGCGGG CCGGGCCCCC	300
ACGCCGGAGG ACTTTCCCCG GCAACTCGCC CTCATCAAGG AGCTGGTGGG CCTCCTGGGG	360
CTGGCGCGCC TCGAGGTCCC GGGCTACGAG GCGGACGACG TCCTGGCCAG CCTGGCCAAG	420
AAGGCGGAAA AGGAGGGCTA CGAGGTCCGC ATCCTCACCG CCGACAAAGA CCTTTACCAG	480
CTTCTTTCCG ACCGCATCCA CGTCCTCCAC CCCGAGGGGT ACCTCATCAC CCCGGCCTGG	540
CTTTGGGAAA AGTACGGCCT GAGGCCCGAC CAGTGGGCCG ACTACCGGGC CCTGACCGGG	600
GACGAGTCCG ACAACCTTCC CGGGGTCAAG GGCATCGGGG AGAAGACGGC GAGGAAGCTT	660
CTGGAGGAGT GGGGGAGCCT GGAAGCCCTC CTCAAGAACC TGGACCGGCT GAAGCCCGCC	720
ATCCGGGAGA AGATCCTGGC CCACATGGAC GATCTGAAGC TCTCCTGGGA CCTGGCCAAG	780
GTGCGCACCG ACCTGCCCCT GGAGGTGGAC TTCGCCAAA GGCGGGAGCC CGACCGGGAG	840
AGGCTTAGGG CCTTTCTGGA GAGGCTTGAG TTTGGCAGCC TCCTCCACGA GTTCGGCCTT	900
CTGGAAAGCC CCAAGGCCGC ACTCGAGCAC CACCACCACC ACCACTGA	948

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGCCAGGGTT TTCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT	60
CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT	120
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG	180
TTTCCTGTGT GAAATTGTTA TCCGCT	206

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTCTGGGTTC TCTGCTCTCT GGTCGCTGTC TCGCTTGTTTC GTC

43

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCTGTCTCGC TTGTTTCGTC

19

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GACGAACAAG CGAGACAGCG

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCTGGGTTC TCTGCTCTCT GGTC

24

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GACGAACAAG CGAGACAGCG ACCAGAGAGC AGAGAACCCA GAA

43

00940925 082801
T082801 52604650

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACCAGAGAGC AGAGAACCCA GAA

23

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACAGCTATG ACCATGATTA C

21

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA

60

TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA

120

GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG

157

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTAGACA TAACCGGGAA

60

TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA

120

GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG

157

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CACCGTCCTC TTCAAGAAG

19

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTGAATCTTG TAGATAGCTA

20

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCCTTATTTT ACTTTAAAAA TTTTCAAATG TTTCTTTTAT ACACAATATG TTTCTTAGTC 60
TGAATAACCT TTTCTCTGTC AGTATTTTTG AGCAGTGGCT CCGAAGGCAC CGTCCTCTTC 120
AAGAAGTTTA TCCAGAAGCC AATGCACCCA TTAGACATAA CCGGGAATCC TACATGGTTC 180
CTTTTATACC ACTGTACAGA AATGGTGATT TCTTTATTTT ATCCAAAGAT CTGGGCTATG 240
ACTATAGCTA TCTACAAGAT TCAGGTAAAG TTTACTTTCT TTCAGAGGAA TTGCTGAATC 300
TAGTGTTACC AATTTATTTT GAGATAACAC AAAACTTTA 339

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCCTTATTTT ACTTTAAAAA T

21

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAAGTTTTG TGTTATCTCA

20

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA 60

TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA 120

GATCTGGGCT ATGACTATAG CTATCTACAA GATTTCAG 157

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC 60

CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTC CCGGTTATGT CCAATGGGTG 120

CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG 157

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 165 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGCGGATAAC AATTTACAC AGGAAACAGC TATGACCATG ATTACGCCAA GCTATTTAGG 60
TGACACTATA GAATACTCAA GCTTGCATGC CTGCAGGTCG ACTCTAGAGG ATCCCCGGGT 120
ACCGAGCTCG AATTCGCCCT ATAGTGAGTC GTATTAGGAT CCGTG 165

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGCCAGGGTT TTCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT 60
CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT 120
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG 180
TTTCCTGTGT GAAATTGTTA TCCGCT 206

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AGCGGATAAC AATTTACAC AGGA 24

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CACGGATCCT AATACGACTC ACTATAGGG 29

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CGCCAGGGTT TTCCAGTCA CGAC

24

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTAGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG	157

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA	60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG	157

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA	60
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TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAGACC CAGACTCTTT TCAAGACTAC	180
ATTAAGTCCT ATTTGGAACA AGCGAGTCGG ATCTGGTCAT GGCTCCTTGG GGCGGCGATG	240
GTAGGGGCCG TCCTCACTGC CCTGCTGGCA GGGCTTGTGA GCTTGCTGTG TCGTCACAAG	300
AGAAAGCAGC TTCCTGAAGA AAAGCAGCCA CTCCTCATGG AGAAAGAGGA TTACCACAGC	360
TTGTATCAGA GCCATTTA	378

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA	60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAGACC CAGACTCTTT TCAAGACTAC	180
ATTAAGTCCT ATTTGGAACA AGCGAGTCGG ATCTGGTCAT GGCTCCTTGG GGCGGCGATG	240
GTAGGGGCCG TCCTCACTGC CCTGCTGGCA GGGCTTGTGA GCTTGCTGTG TCGTCACAAG	300
AGAAAGCAGC TTCCTGAAGA AAAGCAGCCA CTCCTCATGG AGAAAGAGGA TTACCACAGC	360
TTGTATCAGA GCCATTTA	378

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1059 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GCAAGTTTGG CTTTTGGGGA CCAAACGTCA CAGAGAGACG ACTCTTGGTG AGAAGAAACA	60
TCTTCGATTT GAGTGCCCCA GAGAAGGACA AATTTTGTGC CTACCTCACT TTAGCAAAGC	120
ATACCATCAG CTCAGACTAT GTCATCCCCA TAGGGACCTA TGGCCAAATG AAAAATGGAT	180
CAACACCCAT GTTTAACGAC ATCAATATTT ATGACCTCTT TGTCTGGATG CATTATTATG	240
TGTCAATGGA TGCACTGCTT GGGGGATATG AAATCTGGAG AGACATTGAT TTTGCCCATG	300
AAGCACCAGC TTTTCTGCCT TGGCATAGAC TCTTCTTGTT GCGGTGGGAA CAAGAAATCC	360

AGAAGCTGAC AGGAGATGAA AACTTCACTA TTCCATATTG GGACTGGCGG GATGCAGAAA	420
AGTGTGACAT TTGCACAGAT GAGTACATGG GAGGTCAGCA CCCCACAAAT CCTAACTTAC	480
TCAGCCCAGC ATCATTCTTC TCCTCTTGGC AGATTGTCTG TAGCCGATTG GAGGAGTACA	540
ACAGCCATCA GTCTTTATGC AATGGAACGC CCGAGGGACC TTTACGGCGT AATCCTGGAA	600
ACCATGACAA ATCCAGAACC CCAAGGCTCC CCTCTTCAGC TGATGTAGAA TTTTGCCTGA	660
GTTTGACCCA ATATGAATCT GGTTCATGG ATAAAGCTGC CAATTTTCAGC TTTAGAAATA	720
CACTGGAAGG ATTTGCTAGT CCACTTACTG GGATAGCGGA TGCCTCTCAA AGCAGCATGC	780
ACAATGCCTT GCACATCTAT ATGAATGGAA CAATGTCCCA GGTACAGGGA TCTGCCAACG	840
ATCCTATCTT CCTTCTTCAC CATGCATTTG TTGACAGTAT TTTTGAGCAG TGGCTCCGAA	900
GGCACCGTCC TCTTCAAGAA GTTTATCCAG AAGCCAATGC ACCCATTTGGA CATAACCGGG	960
AATCCTACAT GGTTCCTTTT ATACCACTGT ACAGAAATGG TGATTTCTTT ATTTTCATCCA	1020
AAGATCTGGG CTATGACTAT AGCTATCTAC AAGATTCAG	1059

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1059 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCAAGTTTGG CTTTTGGGGA CCAACTGCA CAGAGAGACG ACTCTTGGTG AGAAGAAACA	60
TCTTCGATTT GAGTGCCCCA GAGAAGGACA AATTTTTTGC CTACCTCACT TTAGCAAAGC	120
ATACCATCAG CTCAGACTAT GTCATCCCCA TAGGGACCTA TGGCCAAATG AAAAATGGAT	180
CAACACCCAT GTTTAACGAC ATCAATATTT ATGACCTCTT TGTCTGGATG CATTATTATG	240
TGTCAATGGA TGCCTGCTT GGGGGATATG AAATCTGGAG AGACATTGAT TTTGCCCCATG	300
AAGCACCAGC TTTTCTGCCT TGGCATAGAC TCTTCTTGTT GCGGTGGGAA CAAGAAATCC	360
AGAAGCTGAC AGGAGATGAA AACTTCACTA TTCCATATTG GGACTGGCGG GATGCAGAAA	420
AGTGTGACAT TTGCACAGAT GAGTACATGG GAGGTCAGCA CCCCACAAAT CCTAACTTAC	480
TCAGCCCAGC ATCATTCTTC TCCTCTTGGC AGATTGTCTG TAGCCGATTG GAGGAGTACA	540
ACAGCCATCA GTCTTTATGC AATGGAACGC CCGAGGGACC TTTACGGCGT AATCCTGGAA	600
ACCATGACAA ATCCAGAACC CCAAGGCTCC CCTCTTCAGC TGATGTAGAA TTTTGCCTGA	660
GTTTGACCCA ATATGAATCT GGTTCATGG ATAAAGCTGC CAATTTTCAGC TTTAGAAATA	720
CACTGGAAGG ATTTGCTAGT CCACTTACTG GGATAGCGGA TGCCTCTCAA AGCAGCATGC	780

ACAATGCCTT GCACATCTAT ATGAATGGAA CAATGTCCCA GGTACAGGGA TCTGCCAACG	840
ATCCTATCTT CCTTCTTCAC CATGCATTTG TTGACAGTAT TTTTGAGCAG TGGCTCCGAA	900
GGCACCCTCC TCTTCAAGAA GTTTATCCAG AAGCCAATGC ACCCATTTGA CATAACCAGG	960
AATCCTACAT GGTTCCTTTT ATACCACTGT ACAGAAATGG TGATTTCTTT ATTTTCATCCA	1020
AAGATCTGGG CTATGACTAT AGCTATCTAC AAGATTCAG	1059

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1587 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATGCTCCTGG CTGTTTGTGA CTGCCTGCTG TGGAGTTTCC AGACCTCCGC TGGCCATTTC	60
CCTAGAGCCT GTGTCTCCTC TAAGAACCTG ATGGAGAAGG AATGCTGTCC ACCGTGGAGC	120
GGGGACAGGA GTCCCTGTGG CCAGCTTTCA GGCAGAGGTT CCTGTCAGAA TATCCTTCTG	180
TCCAATGCAC CACTTGGGCC TCAATTTCCTC TTCACAGGGG TGGATGACCG GGAGTCGTGG	240
CCTTCCGTCT TTTATAATAG GACCTGCCAG TGCTCTGGCA ACTTCATGGG ATTCAACTGT	300
GGAAACTGCA AGTTTGGCTT TTGGGGACCA AACTGCACAG AGAGACGACT CTTGGTGAGA	360
AGAAACATCT TCGATTTGAG TGCCCCAGAG AAGGACAAAT TTTTTCCTTA CCTCACTTTA	420
GCAAAGCATA CCATCAGCTC AGACTATGTC ATCCCCATAG GGACCTATGG CCAAATGAAA	480
AATGGATCAA CACCCATGTT TAACGACATC AATATTTATG ACCTCTTTGT CTGGATGCAT	540
TATTATGTGT CAATGGATGC ACTGCTTGGG GGATATGAAA TCTGGAGAGA CATTGATTTT	600
GCCCATGAAG CACCAGCTTT TCTGCCTTGG CATAGACTCT TCTTGTGCG GTGGGAACAA	660
GAAATCCAGA AGCTGACAGG AGATGAAAAC TTCACTATTC CATATTGGGA CTGGCGGGAT	720
GCAGAAAAGT GTGACATTTG CACAGATGAG TACATGGGAG GTCAGCACCC CACAAATCCT	780
AACTTACTCA GCCCAGCATC ATTCTTCTCC TCTTGGCAGA TTGTCTGTAG CCGATTGGAG	840
GAGTACAACA GCCATCAGTC TTTATGCAAT GGAACGCCCC AGGGACCTTT ACGGCGTAAT	900
CCTGGAAACC ATGACAAATC CAGAACCCCA AGGCTCCCCT CTTCAGCTGA TGTAGAATTT	960
TGCTTGAGTT TGACCCAATA TGAATCTGGT TCCATGGATA AAGCTGCCAA TTTCAGCTTT	1020
AGAAATACAC TGGAAGGATT TGCTAGTCCA CTTACTGGGA TAGCGGATGC CTCTCAAAGC	1080
AGCATGCACA ATGCCCTGCA CATCTATATG AATGGAACAA TGTCCAGGT ACAGGGATCT	1140
GCCAACGATC CTATCTTCCT TCTTCACCAT GCATTTGTTG ACAGTATTTT TGAGCAGTGG	1200

F08280-52504660

CTCCGAAGGC ACCGTCCTCT TCAAGAAGTT TATCCAGAAG CCAATGCACC CATTGGACAT	1260
AACCGGGAAT CCTACATGGT TCCTTTTATA CCACTGTACA GAAATGGTGA TTTCTTTATT	1320
TCATCCAAAG ATCTGGGCTA TGACTATAGC TATCTACAAG ATTCAGACCC AGACTCTTTT	1380
CAAGACTACA TTAAGTCCTA TTTGGAACAA GCGAGTCGGA TCTGGTCATG GCTCCTTGGG	1440
GCGGCGATGG TAGGGGCCGT CCTCACTGCC CTGCTGGCAG GGCTTGTGAG CTTGCTGTGT	1500
CGTCACAAGA GAAAGCAGCT TCCTGAAGAA AAGCAGCCAC TCCTCATGGA GAAAGAGGAT	1560
TACCACAGCT TGTATCAGAG CCATTTA	1587

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1587 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATGCTCCTGG CTGTTTGTGA CTGCCTGCTG TGGAGTTTCC AGACCTCCGC TGGCCATTTC	60
CCTAGAGCCT GTGTCTCCTC TAAGAACCTG ATGGAGAAGG AATGCTGTCC ACCGTGGAGC	120
GGGGACAGGA GTCCCTGTGG CCAGCTTCA GGCAGAGGTT CCTGTCAGAA TATCCTTCTG	180
TCCAATGCAC CACTTGGGCC TCAATTTCCC TTCACAGGGG TGGATGACCG GGAGTCGTGG	240
CCTTCCGTCT TTTATAATAG GACCTGCCAG TGCTCTGGCA ACTTCATGGG ATTCAACTGT	300
GGAAACTGCA AGTTTGGCTT TTGGGGACCA AACTGCACAG AGAGACGACT CTTGGTGAGA	360
AGAAACATCT TCGATTTGAG TGCCCCAGAG AAGGACAAAT TTTTGCCTA CCTCACTTTA	420
GCAAAGCATA CCATCAGCTC AGACTATGTC ATCCCCATAG GGACCTATGG CCAAATGAAA	480
AATGGATCAA CACCCATGTT TAACGACATC AATATTTATG ACCTCTTTGT CTGGATGCAT	540
TATTATGTGT CAATGGATGC ACTGCTTGGG GGATATGAAA TCTGGAGAGA CATTGATTTT	600
GCCCATGAAG CACCAGCTTT TCTGCCTTGG CATAGACTCT TCTTGTTGCG GTGGGAACAA	660
GAAATCCAGA AGCTGACAGG AGATGAAAAC TTCACTATTC CATATTGGGA CTGGCGGGAT	720
GCAGAAAAGT GTGACATTTG CACAGATGAG TACATGGGAG GTCAGCACCC CACAAATCCT	780
AACTTACTCA GCCCAGCATC ATTCTTCTCC TCTTGGCAGA TTGTCTGTAG CCGATTGGAG	840
GAGTACAACA GCCATCAGTC TTTATGCAAT GGAACGCCCC AGGGACCTTT ACGGCGTAAT	900
CCTGGAAACC ATGACAAATC CAGAACCCCA AGGCTCCCCT CTTCAGCTGA TGTAGAATTT	960
TGCCTGAGTT TGACCCAATA TGAATCTGGT TCCATGGATA AAGCTGCCAA TTTCAGCTTT	1020
AGAAATACAC TGGAAGGATT TGCTAGTCCA CTTACTGGGA TAGCGGATGC CTCTCAAAGC	1080

103230-52604660

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC	60
CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTC CCGGTTATGT CTAATGGGTG	120
CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG	157

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC	60
CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTC CTGGTTATGT CCAATGGGTG	120
CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG	157

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GGTTGGCCAA TCTACTCCCA GG	22
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(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCTCACTCAG TGTGGCAAAG	20
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(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCCTGACT CTCTCTGCCT ATTGGTCTAT TTTCCACCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA TCTGACTCCT GAGGAGGTCT GCCGTTACTG CCCTGTGGGG	180
CAAGGTGAAC GTGGATGAAG TTGGTGGTGA GGCCCTGGGC AGGTTGGTAT CAAGGTTACA	240
AGACAGGTTT AAGGAGACCA ATAGAAACTG GGCATGTGGA GACAGAGAAG ACTCTTGGGT	300
TTCTGATAGG CACTGACTCT CTCTGCCTAT TGGTCTATTT TCCCACCCTT AGGCTGCTGG	360
TGGTCTACCC TTGGACCCAG AGGTTCTTTG AGTCCTTTGG GGATCTGTCC ACTCCTGATG	420
CTGTTATGGG CAACCCTAAG GTGAAGGCTC ATGGCAAGAA AGTGCTCGGT GCCTTTAGTG	480
ATGGCCTGGC TCACCTGGAC AACCTCAAGG GCACCTTTGC CACACTGAGT GAGC	534

(2) INFORMATION FOR SEQ ID NO:71:

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GAAUACUCAA GCUUGCAUGC CUGCAGGU CG ACUCUAGAGG AUCCCCGGGU ACCGAGCUCG 60
AAUU 64

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GGCTGACAAG AAGGAAACTC 20

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCAGGCGGCG GCTAGGAGAG ATGGG 25

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG 60
GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCACTCTCT TGATGTATAA ATATCACTGC 120
ATTTGCTCT GTATTCAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTC 180
TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC 240
CGGTGCTGGG CAGAGTGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC 300

ATTTTAGAAG TAGGCCAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G

351

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGCTGACAAG AAGGAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG	60
GAGGAGCCGG TCGGGAACAC CCACTTTCTT GATGTATAAA TATCACTGCA TTTCGCTCTG	120
TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT	180
AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTCACCA GCACTTAGCC AGTGCTGGGC	240
AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTTAGAAGT	300
AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG	340

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GGCTGACAAG AAGGAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG	60
GAGGAGCCGG TCGGGAACAC CCACTTTCTT GGTGTATAAA TATCACTGCA TTTCGCTCTG	120
TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT	180
AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTCACCA GCACTTGGCC AGTGCTGGGC	240
AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTTAGAAGT	300
AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG	340

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG 60
 GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCCCTCTCT TGATGTATAA ATATCACTGC 120
 ATTTGCTCT GTATTCAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTC 180
 TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC 240
 CGGTGCTGGG CAGAGTGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC 300
 ATTTTAGAAG TAGGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G 351

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GGCTGACAAG AAGGAAACTC GCTGAAACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG 60
 GAGGTACTGG GAAGGAGCCG GTCGGGAACG CCCACTTTCT TGATGTATAA ATATCACTGC 120
 ATTTGCTCT GTATTCAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTC 180
 TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC 240
 CGGTGCTGGG CAGAGTGA CT CCACGCTTGC TTGCTTAAAG CCCTCTTCAA TAAAGCTGCC 300
 ATTTTAGAAG TAAGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G 351

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGA 60
 GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCACTCTCT TGATGTATAA ATATCACTGC 120
 ATTTGCTCT GTATTCAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TAGGAGGTTC 180
 TCTCCAGCAC TAGCAGGTAG AGCCTGAGTG TTCCCTGCTA AACTCTCACC AGCACTTGGC 240
 CGGTGCTGGG CAGAGCGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC 300
 ATTTTAGAAG TAGGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G 351

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA TCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT AAGGCCCTGG GCAGGTTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCAGTGA CTCTCTGCCT ATTGGTCTAT TTTCCACCCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCAGTGA CTCTCTGCCT ATTAGTCTAT TTTCCACCCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA	60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG	157

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 833 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu	15
1 5 10	
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys	30
20 25 30	
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe	45
35 40 45	
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile	60
50 55 60	
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly	80
65 70 75 80	
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln	95
85 90 95	
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu	110
100 105 110	
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys	125
115 120 125	
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys	140
130 135 140	
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu	160
145 150 155 160	
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg	175
165 170 175	
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp	190
180 185 190	

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Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
405 410 415

Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
450 455 460

Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750

Pro Val Arg Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 548 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	20	25	30	
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	195	200	205	
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220	
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	225	230	235	240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	245	250	255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	260	265	270	
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	275	280	285	

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Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
405 410 415

Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
450 455 460

Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525

Ile Val Glu Lys Ile Leu Gln Ala Cys Lys Leu Gly Thr Gly Arg Arg
530 535 540

Phe Thr Thr Ser
545

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 695 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

108230" 52604660

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	20	25	30	
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	195	200	205	
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220	
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	225	230	235	240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	245	250	255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	260	265	270	
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	275	280	285	
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	290	295	300	
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	305	310	315	320
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	325	330	335	

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Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
405 410 415

Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
450 455 460

Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ser His Pro Leu
675 680 685

Arg Gly Gly Pro Gly Leu His
690 695

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	20	25	30	
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	195	200	205	
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220	
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	225	230	235	240

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Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly
195 200 205

Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp
210 215 220

Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala
225 230 235 240

Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp
245 250 255

Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala
260 265 270

Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg
275 280 285

Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro
290 295 300

Lys Ser Trp Arg Gly Cys Ile Pro Trp Pro Cys Pro Trp Arg Trp Arg
305 310 315 320

Trp Gly

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 528 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly
1 5 10 15

His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr
20 25 30

Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu
35 40 45

Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp
50 55 60

Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala
65 70 75 80

Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile
85 90 95

Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly
100 105 110

Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys
115 120 125

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Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln
130 135 140

Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile
145 150 155 160

Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp
165 170 175

Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly
180 185 190

Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp
195 200 205

Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala
210 215 220

Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp
225 230 235 240

Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala
245 250 255

Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg
260 265 270

Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro
275 280 285

Lys Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala
290 295 300

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
305 310 315 320

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
325 330 335

Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro
340 345 350

Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
355 360 365

Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
370 375 380

Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
385 390 395 400

Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
405 410 415

Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg
420 425 430

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
435 440 445

Val Arg Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
450 455 460

Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp
 210 215 220

Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala
 225 230 235 240

Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp
 245 250 255

Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala
 260 265 270

Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg
 275 280 285

Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro
 290 295 300

Lys Ala Ala Leu Glu His His His His His His
 305 310 315

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTTCA	60
GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG	120
GATGATTTGA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA	180
GATGAAGCTC CCAGAATGCC AGAGGCTGCT CCCCCCGTGG CCCCTGCACC AGCAGCTCCT	240
ACACCGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCCCTGT CATCTTCTGT CCCTTCCCAG	300
AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG	360
TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAGATGT TTTGCCAACT GGCCAAGACC	420
TGCCCTGTGC AGCTGTGGGT TGATTCCACA CCCCCGCCCC GCACCCGCGT CCGCGCCATG	480
GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GGCCTGCCC CCACCATGAG	540
CGCTGCTCAG ATAGCGATGG TCTGGCCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT	600
TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTTCGAC ATAGTGTGGT GGTGCCCTAT	660
GAGCCGCTG AGGTTGGCTC TGA CTGTACC ACCATCCACT ACAACTACAT GTGTAACAGT	720
TCCTGCATGG GCGGCATGAA CCGGAGGCCC ATCCTCACCA TCATCACACT GGAAGACTCC	780
AGTGGAATC TACTGGGACG GAACAGCTTT GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA	840
GACCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCCC	900

CCAGGGAGCA CTAAGCGAGC ACTGCCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG	960
AAACCACTGG ATGGAGAATA TTTCACCCCTT CAGATCCGTG GCGGTGAGCG CTTCGAGATG	1020
TTCCGAGAGC TGAATGAGGC CTTGGAAGTC AAGGATGCCC AGGCTGGGAA GGAGCCAGGG	1080
GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAAGG GTCAGTCTAC CTCCCGCCAT	1140
AAAAAACTCA TGTTCAGAC AGAAGGGCCT GACTCAGACT GA	1182

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTTCA	60
GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG	120
GATGATTTGA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA	180
GATGAAGCTC CCAGAATGCC AGAGGCTGCT CCCCCCGTGG CCCCTGCACC AGCAGCTCCT	240
ACACCGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCCGTG CATCTTCTGT CCCTTCCCAG	300
AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCAATTCTGG GACAGCCAAG	360
TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAGATGT TTTGCCAACT GGCCAAGACC	420
TGCCCTGCGC AGCTGTGGGT TGATTCCACA CCCCCGCCG GCACCCGCGT CCGCGCCATG	480
GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GCGCTGCCC CCACCATGAG	540
CGCTGCTCAG ATAGCGATGG TCTGGCCCCT CTCAGCATC TTATCCGAGT GGAAGGAAAT	600
TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTTCGAC ATAGTGTGGT GGTGCCCTAT	660
GAGCCGCTG AGGTTGGCTC TGAAGTACC ACCATCCACT ACAACTACAT GTGTAACAGT	720
TCCTGCATGG GCGGCATGAA CCGGAGGCCC ATCCTCACCA TCATCACACT GGAAGACTCC	780
AGTGGAATC TACTGGGACG GAACAGCTTT GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA	840
GACCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCCC	900
CCAGGGAGCA CTAAGCGAGC ACTGCCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG	960
AAACCACTGG ATGGAGAATA TTTCACCCCTT CAGATCCGTG GCGGTGAGCG CTTCGAGATG	1020
TTCCGAGAGC TGAATGAGGC CTTGGAAGTC AAGGATGCCC AGGCTGGGAA GGAGCCAGGG	1080
GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAAGG GTCAGTCTAC CTCCCGCCAT	1140
AAAAAACTCA TGTTCAGAC AGAAGGGCCT GACTCAGACT GA	1182

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTTCA	60
GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG	120
GATGATTTGA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA	180
GATGAAGCTC CCAGAATGCC AGAGGCTGCT CCCCCGTGG CCCCTGCACC AGCAGCTCCT	240
ACACCGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCCGTGT CATCTTCTGT CCCTTCCCAG	300
AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG	360
TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAAGATGT TTTGCCAACT GGCCAAGACC	420
TGCCCTGTGC AGCTGTGGGT TGATTCCACA CCCCCGCCCC GCACCCGCGT CCGCGCCATG	480
GCCATCTACA AGCAGTCACA GCACATGACG GAGGTGTGA GCGCTGCCC CCACCATGAG	540
CGCTGCTCAG ATAGCGATGG TCTGGCCCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT	600
TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT	660
GAGCCGCCTG AGGTGGCTC TGA CTGTG TACC ACCATCCACT ACAACTACAT GTGTAACAGT	720
TCCTGCATGG GCGGCATGAA CCGGAGACCC ATCCTCACCA TCATCACACT GGAAGACTCC	780
AGTGGAATC TACTGGGACG GAACAGCTTT GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA	840
GACCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCCC	900
CCAGGGAGCA CTAAGCGAGC ACTGCCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG	960
AAACCACTGG ATGGAGAATA TTTCACCCTT CAGATCCGTG GCGTGAGCG CTTGAGATG	1020
TTCCGAGAGC TGAATGAGGC CTTGGAATC AAGGATGCC AGGCTGGGAA GGAGCCAGGG	1080
GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAAGG GTCAGTCTAC CTCCCGCCAT	1140
AAAAAACTCA TGTTC AAGAC AGAAGGGCCT GACTCAGACT GA	1182

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TCTGGGCTTC TTGCATTCTG

20

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTTGGGCAGT GCTCGCTTAG

20

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT 60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC 120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC 180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC 240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA 300
CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC 360
CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC 420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT 480
TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG 540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA 600
C 601

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTGCGGCAGT GCTCGCTTAG TGCTCCCTGG GGCAGCTCG TGGTGAGGCT CCCCTTTCTT 60
GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC 120
AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT 180
GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT 240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT 300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG 360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGCAGCGCC TCACAACCTC 420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG 480
TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAA ACATCTTGTT 540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG 600
A 601

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT 60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGCG CAGCTGTGGG TTGATTCCAC 120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC 180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC 240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA 300
CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCTT GAGGTTGGCT CTGACTGTAC 360
CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GGCAGCATGA ACCGGAGGCC 420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGAAT CTACTGGGAC GGAACAGCTT 480
TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG 540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA 600
C 601

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCAGGA CAGGCACAAA CACGCACCTC	120
AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG	480
TGTGGAATCA ACCCACAGCT GCGCAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTT	540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG	600
A	601

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 601 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGACC	420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA	600

C

601

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 601 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GT TGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT 60
GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCAGGA CAGGCACAAA CACGCACCTC 120
AAAGCTGTTC CGTCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT 180
GGGTCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT 240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT 300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCCCTTCC ACTCGGATAA GATGCTGAGG 360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC 420
CGTCATGTGC TGTGACTGCT TG TAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG 480
TGTGGAATCA ACCCAGCT GCACAGGGCA GGTCTTGCC AGTTGGCAAA ACATCTTGTT 540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG 600
A 601

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GAGGATGGGA CTCCGGTTCA TG 22

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CATGAACCGG AGTCCCATCC TCAC

24

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GCACAAACAT GCACCTCAAA GCT

23

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CAGCTTTGAG GTGCATGTTT GT

22

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GCGGCGATGA ACCGGAGTCC	420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA	600

C

601

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 601 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT 60
 GCGGAGATTG TCTTCCTCTG TGCGCCGGTC TCTCCAGGA CAGGCACAAA CACGCACCTC 120
 AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT 180
 GGGACTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT 240
 GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT 300
 GTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG 360
 AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC 420
 CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG 480
 TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTT 540
 GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG 600
 A 601

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 601 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT 60
 CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC 120
 ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC 180
 GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC 240
 TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA 300
 CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC 360
 CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC 420

09940925 032301
103230 "5260450

CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCAT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTGCGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCAGGA CAGGCACAAA CATGCACCTC	120
AAAGCTGTTC CGTCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG	480
TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTT	540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG	600
A	601

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240

TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GCGGCATGA ACCGGAGTCC	420
CATCCTC	427

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATGAACCGG AGTCCCATCC TCACCATCAT CACACTGGAA GACTCCAGTG GTAATCTACT	60
GGGACGGAAC AGCTTTGAGG TGCGTGTTTG TGCCTGTCCT GGGAGAGACC GGCACACAGA	120
GGAAGAGAAT CTCCGCAAGA AAGGGGAGCC TCACCACGAG CTGCCCCCAG GGAGCACTAA	180
GCGAGCACTG CCCAAC	196

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GCGGCATGA ACCGGAGGCC	420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCAT GTTTGTGC	498

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CAGCTTTGAG GTGCATGTTT GTGCCTGTCC TGGGAGAGAC CGGCGCACAG AGGAAGAGAA 60
TCTCCGCAAG AAAGGGGAGC CTCACCACGA GCTGCCCCCA GGGAGCACTA AGCGAGCACT 120
GCCCAAC 127

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GGTTTTTCTT TGAGGTTTAG 20

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GCGACACTCC ACCATAGAT 19

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CTGTCTTCAC GCAGAAAGC 19

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

09940595-082801
108280-52504660

09440925-032301
102230-52504560

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GCACGGTCTA CGAGACCTC

19

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GATCTACTAG TCATATGGAT

20

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TCGGTACCCG GGGATCCGAT

20

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CTGTCTTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG

60

GACCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC

120

CAGGACGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG CCTGGAGATT TGGGCGTGCC

180

CCCGCAAGAC TGCTAGCCGA GTAGTGTGG GTCGCGAAAG GCCTTGTGGT ACTGCCTGAT

240

AGGGTGCCTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C

281

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CTGTCTTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG	60
GACCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGACTGTC TTCACGCAGA	120
AAGCGTCTAG CCATGGCGTT AGTATGAGTG TCGTGCAGCC TCCAGGACCC CCCCTCCCGG	180
GAGAGCCATA GTGGTCTGCG GAACCGGTGA GTACACCGGA ATTGCCAGGA CGACCGGGTC	240
CTTTCTTGA TCAACCGCT CAATGCCTGG AGATTGGGC GTGCCCCGC AAGACTGCTA	300
GCCGAGTAGT GTTGGGTCGC GAAAGGCCTT GTGGTACTGC CTGATAGGGT GCTTGCAGT	360
GCCCCGGGAG GTCTCGTAGA CCGTGC	386

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG	60
GTCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CAGGACGACC GGGTCCTTTC TTGGATCAAC CCGCTCAATG CCTGGAGATT TGGGCGTGCC	180
CCCGCGAGAC TGCTAGCCGA GTAGTGTTGG GTCGCGAAAG GCCTTGTGGT ACTGCCTGAT	240
AGGGTGCTTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C	281

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG	60
GACCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CAGGACGACC GGGTCCTTTC GTGGATGTAA CCGCTCAAT GCCTGGAGAT TTGGGCGTGC	180

CCCCGCAAGA CTGCTAGCCG AGTAGTGTG GGTGCGGAAA GGCCTTGTGG TACTGCCTGA 240
TAGGGTGCTT GCGAGTGCCC CGGGAGGTCT CGTAGACCGT GC 282

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTGCGTA CAGCCTCCAG 60
GCCCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC 120
CGGGAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG CCCGGCCATT TGGGCGTGCC 180
CCCCGAAGAC TGCTAGCCGA GTAGCGTTGG GTTGCAGAAAG GCCTTGTGGT ACTGCCTGAT 240
AGGGTGCTTG CGAGTACCCC GGGAGGTCTC GTAGACCGTG C 281

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTGTCTTCAC GCAGAAAGCG CCTAGCCATG GCGTTAGTAC GAGTGTGCGTG CAGCCTCCAG 60
GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC 120
TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA CCCAGAAATT TGGGCGTGCC 180
CCCGCGAGAT CACTAGCCGA GTAGTGTGG GTGCGGAAAG GCCTTGTGGT ACTGCCTGAT 240
AGGGTGCTTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C 281

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAGGCACCC TATCAGGCAG TACCACAAGG 60

CCTTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATCTCCAG	120
GCATTGAGCG GGTTTATCCA AGAAAGGACC CGGTCGTCCT GGCAATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT	240
CATACTAACG CCATGGCCAG ACGCTTTCTG CGTGAAGACA G	281

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATCTCCAG	120
GCATTGAGCG GGTTGATCCA AGAAAGGACC CGGTCGTCCT GGCAATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT	240
CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G	281

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTCGCGG GGGCACGCCC AAATCTCCAG	120
GCATTGAGCG GGTTGATCCA AGAAAGGACC CGGTCGTCCT GGCAATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGA CCTGGAGGCT GCACGACACT	240
CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G	281

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG 60
CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATCTCCAG 120
GCATTGAGCG GGTACATCC ACGAAAGGAC CCGGTCGTCC TGGCAATTCC GGTGTACTCA 180
CCGGTTCCGC AGACCACTAT GGCTCTCCCG GGAGGGGGGG TCCTGGAGGC TGCACGACAC 240
TCATACTAAC GCCATGGCTA GACGCTTTCT GCGTGAAGAC AG 282

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCACGGTCTA CGAGACCTCC CGGGGTACTC GCAAGCACCC TATCAGGCAG TACCACAAGG 60
CCTTTCGCAA CCCAACGCTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATGGCCGG 120
GCATAGAGTG GGTATTATCCA AGAAAGGACC CAGTCTTCCC GGCAATTCCG GTGTACTCAC 180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGG CCTGGAGGCT GTACGACACT 240
CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G 281

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG 60
CCTTTCGCGA CCCAACACTA CTCGGCTAGT GATCTCGCGG GGGCACGCCC AAATTTCTGG 120
GTATTGAGCG GGTGCTCCA AGAAAGGACC CCGTCACCCC AGCGATTCCG GTGTACTCAC 180
CCGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT 240
CGTACTAACG CCATGGCTAG GCGCTTTCTG CGTGAAGACA G 281

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ATCAACATCC GGCCGGTGGT

20

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GGGGCCTCGC TACGGACCAG

20

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 620 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ATCAACATCC GGCCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC 60

CAATTCATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCC ACAAGCGCCG ACTGTCGGCG 120

CTGGGGCCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG 180

TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC 240

GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTTCGGGT TCATCGAAAC GCCGTACCGC 300

AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC 360

CGCCACGTGG TGGCACAGGC CAATTCGCCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG 420

CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC 480

TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG 540

GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GCGGGTGCCG 600

CTGGTCCGTA GCGAGGCCCC 620

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 620 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

ATCAACATCC GGCCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC 60
CAATTCATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCT ACAAGCGCCG ACTGTCGGCG 120
CTGGGGCCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG 180
TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC 240
GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTTCGGGT TCATCGAAAC GCCGTACCGC 300
AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC 360
CGCCACGTGG TGGCACAGGC CAATTCGCCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG 420
CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC 480
TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG 540
GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG 600
CTGGTCCGTA GCGAGGCCCC 620

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ATCAACATCC GGCCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC 60
CAATTCATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCC ACAAGCGCCG ACTGTTGGCG 120
CTGGGGCCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG 180
TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC 240
GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTTCGGGT TCATCGAAAC GCCGTACCGC 300
AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC 360
CGCCACGTGG TGGCACAGGC CAATTCGCCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG 420
CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC 480
TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG 540
GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG 600
CTGGTCCGTA GCGAGGCCCC 620

0994095-082801
108280-5260450

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA	60
CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG	120
CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCCGCC	180
TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG	240
GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTGCTA	300
ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC	360
GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG	420
CACATCCGGC CGTAGTGCGA CGGGTGACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT	480
GACAGACCGC CGGGCCCCAG CGCCGACAGT CGGCGCTTGT GGGTCAACCC CGACAGCGGG	540
TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGGCG	600
ACCACCGGCC GGATGTTGAT	620

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA	60
CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG	120
CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCCGCC	180
TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG	240
GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTGCTA	300
ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC	360
GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG	420
CACATCCGGC CGTAGTGCGA CGGGTGACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT	480

09040925 08280 52504650

GACAGACCGC CGGGCCCCAG CGCCGACAGT CGGCGCTTGT AGGTCAACCC CGACAGCGGG 540
 TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGGCG 600
 ACCACCGGCC GGATGTTGAT 620

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA 60
 CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG 120
 CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCCGCC 180
 TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG 240
 GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA 300
 ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC 360
 GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG 420
 CACATCCGGC CGTAGTGCGA CGGGTGACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT 480
 GACAGACCGC CGGGCCCCAG CGCCAACAGT CGGCGCTTGT GGGTCAACCC CGACAGCGGG 540
 TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGGCG 600
 ACCACCGGCC GGATGTTGAT 620

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AGCTCGTATG GCACCGGAAC 20

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTGACCTCCC ACCCGACTTG

20

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA GCGGCATCGA GGTCGTATGG 60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG 120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC 180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC 240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC 300
GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT 360
CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG 420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG 480
ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG 540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA 600
CAAGTCGGGT GGGAGGTCAA 620

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CCGGCATCGA GGTCGTATGG 60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG 120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC 180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC 240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC 300

GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT 360
 CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG 420
 GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG 480
 ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG 540
 TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA 600
 CAAGTCGGGT GGGAGGTCAA 620

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 620 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA GCGGCATCGA GGTCGTATGG 60
 ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG 120
 GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC 180
 GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC 240
 CTCTCGCTGC GGGTGGATCC GATCTATGAG CCGATCACGC GTCGCTGGCT GGAACACCCC 300
 GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT 360
 CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG 420
 GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG 480
 ATCCTGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG 540
 TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA 600
 CAAGTCGGGT GGGAGGTCAA 620

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 620 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CCGGCATCGA GGTCGTATGG 60
 ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG 120

GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC	180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC	240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC	300
GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT	360
CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG	420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG	480
ATCCTGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG	540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA	600
CAAGTCGGGT GGGAGGTCAA	620

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC	60
TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA	120
GTCAATCCCG ATGCCCCGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG	180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC	240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG	300
AACTCGTCGG CCAATTCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC	360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG	420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA	480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTTCTGTCG GGGTGTTCTG CCATACGACC TCGATGCCGC TGGTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATACGAGCT	620

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC	60
TTGTGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA	120
GTCAATCCCG ATGCCCGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG	180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC	240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG	300
AACTCGTCGG CCAATTCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC	360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG	420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA	480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTTGTCG GGGTGTTCGT CCATACGACC TCGATGCCG TGGTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATAAGAGCT	620

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC	60
TTGTGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA	120
GTCAATCCCG ATGCCCGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG	180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC	240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG	300
AACTCGTCGG CCAATTCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC	360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG	420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA	480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTTGTCG GGGTGTTCGT CCATACGACC TCGATGCCG TGGTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATAAGAGCT	620

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC	60
TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA	120
GTCAATCCCG ATGCCAGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG	180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC	240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG	300
AACTCGTCGG CCAATTCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC	360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG	420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA	480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGG TGGTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATACGAGCT	620

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGAGTTTGAT CCTGGCTCAG	20
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(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GGCGGACGGG TGAGTAA	17
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(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CTGCTGCCTC CCGTAGGAGT

20

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATGACGTCAA GTCATCATGG CCCTTACGA

29

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTACAAGGCC CGGGAACGTA TTCACCG

27

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GCAACGAGCG CAACCC

16

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ATGACGTCAA GTCATCATGG CCCTTA

26

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1542 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

AAATTGAAGA GTTTGATCAT GGCTCAGATT GAACGCTGGC GGCAGGCCTA ACACATGCAA 60
GTCGAACGGT AACAGGAAGA AGCTTGCTTC TTTGCTGACG AGTGGCGGAC GGGTGAGTAA 120
TGTCTGGGAA ACTGCCTGAT GGAGGGGGAT AACTACTGGA AACGGTAGCT AATACCGCAT 180
AACGTCGCAA GACCAAAGAG GGGGACCTTC GGGCCTCTTG CCATCGGATG TGCCCAGATG 240
GGATTAGCTA GTAGGTGGGG TAACGGCTCA CCTAGGCGAC GATCCCTAGC TGGTCTGAGA 300
GGATGACCAG CCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTGG 360
GGAATATTGC ACAATGGGCG CAAGCCTGAT GCAGCCATGC CGCGTGTATG AAGAAGGCCT 420
TCGGGTTGTA AAGTACTTTC AGCGGGGAGG AAGGGAGTAA AGTTAATACC TTTGCTCATT 480
GACGTTACCC GCAGAAGAAG CACCGGCTAA CTCCGTGCCA GCAGCCGCGG TAATACGGAG 540
GGTGCAAGCG TTAATCGGAA TTAAGGCGC TAAAGCGCAC GCAGGCGGTT TGTAAAGTCA 600
GATGTGAAAT CCCCGGGCTC AACCTGGGAA CTGCATCTGA TACTGGCAAG CTTGAGTCTC 660
GTAGAGGGGG GTAGAATTCC AGGTGTAGCG GTGAAATGCG TAGAGATCTG GAGGAATACC 720
GGTGGCGAAG GCGGCCCCCT GGACGAAGAC TGACGCTCAG GTGCGAAAGC GTGGGGAGCA 780
AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT GTCGACTTGG AGGTTGTGCC 840
CTTGAGGCGT GGCTTCCGGA GCTAACGCGT TAAGTCGACC GCCTGGGGAG TACGGCCGCA 900
AGGTTAAAAC TCAAATGAAT TGACGGGGGC CCGCACAAGC GGTGGAGCAT GTGGTTTAAT 960
TCGATGCAAC GCGAAGAACC TTACCTGGTC TTGACATCCA CGGAAGTTTT CAGAGATGAG 1020
AATGTGCCTT CGGGAACCGT GAGACAGGTG CTGCATGGCT GTCGTCAGCT CGTGTTGTGA 1080
AATGTTGGGT TAAGTCCCGC AACGAGCGCA ACCCTTATCC TTTGTTGCCA GCGGTCCGGC 1140
CGGGAACCTCA AAGGAGACTG CCAGTGATAA ACTGGAGGAA GGTGGGGATG ACGTCAAGTC 1200
ATCATGGCCC TTACGACCAG GGCTACACAC GTGCTACAAT GGCGCATACA AAGAGAAGCG 1260
ACCTCGCGAG AGCAAGCGGA CCTCATAAAG TGCCTCGTAG TCCGGATTGG AGTCTGCAAC 1320
TCGACTCCAT GAAGTCGGAA TCGCTAGTAA TCGTGGATCA GAATGCCACG GTGAATACGT 1380

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TCCCGGGCCT TGTACACACC GCCCGTCACA CCATGGGAGT GGGTTGCAAA AGAAGTAGGT 1440
 AGCTTAACCT TCGGGAGGGC GCTTACCACT TTGTGATTCA TGACTGGGGT GAAGTCGTAA 1500
 CAAGGTAACC GTAGGGGAAC CTGCGGTTGG ATCACCTCCT TA 1542

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

TTTTTATGGA GAGTTTGATC CTGGCTCAGA GTGAACGCTG GCGGCGTGCC TAATACATGC 60
 AAGTCGAACG ATGAAGCTTC TAGCTTGCTA GAAGTGGATT AGTGGCGCAC GGGTGAGTAA 120
 GGTATAGTTA ATCTGCCCTA CACAAGAGGA CAACAGTTGG AAACGACTGC TAATACTCTA 180
 TACTCCTGCT TAACACAAGT TGAGTAGGGA AAGTTTTTCG GTGTAGGATG AGACTATATA 240
 GTATCAGCTA GTTGGTAAGG TAATGGCTTA CCAAGGCTAT GACGCTTAAC TGGTCTGAGA 300
 GGATGATCAG TCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTAG 360
 GGAATATTGC GCAATGGGGG AAACCCTGAC GCAGCAACGC CGCGTGGAGG ATGACACTTT 420
 TCGGAGCGTA AACTCCTTTT CTTAGGGAAG AATTCTGACG GTACCTAAGG AATAAGCACC 480
 GGCTAACTCC GTGCCAGCAG CCGCGGTAAT ACGGAGGGTG CAAGCGTTAC TCGGAATCAC 540
 TGGGCGTAAA GGGCGCGTAG GCGGATTATC AAGTCTCTTG TGAAATCTAA TGGCTTAACC 600
 ATTAACTGC TTGGGAAACT GATAGTCTAG AGTGAGGGAG AGGCAGATGG AATTGGTGGT 660
 GTAGGGGTAA AATCCGTAGA TATCACCAAG AATACCCATT GCGAAGGCGA TCTGCTGGAA 720
 CTCAACTGAC GCTAAGGCGC GAAAGCGTGG GGAGCAAACA GGATTAGATA CCCTGGTAGT 780
 CCACGCCCTA AACGATGTAC ACTAGTTGTT GGGGTGCTAG TCATCTCAGT AATGCAGCTA 840
 ACGCATTAAG TGTACCGCCT GGGGAGTACG GTCGCAAGAT TAAAACTCAA AGGAATAGAC 900
 GGGGACCCGC ACAAGCGGTG GAGCATGTGG TTTAATTCGA AGATACGCGA AGAACCTTAC 960
 CTGGGCTTGA TATCCTAAGA ACCTTTTAGA GATAAGAGGG TGCTAGCTTG CTAGAACTTA 1020
 GAGACAGGTG CTGCACGGCT GTCGTCAGCT CGTGTCGTGA GATGTTGGGT TAAGTCCCGC 1080
 AACGAGCGCA ACCCACGTAT TTAGTTGCTA ACGGTTCCGC CGAGCACTCT AAATAGACTG 1140
 CCTTCGTAAG GAGGAGGAAG GTGTGGACGA CGTCAAGTCA TCATGGCCCT TATGCCCAGG 1200
 GCGACACACG TGCTACAATG GCATATAGAA TGAGACGCAA TACCGCGAGG TGGAGCAAAT 1260
 CTATAAAATA TGTCCCAGTT CGGATTGTTC TCTGCAACTC GAGAGCATGA AGCCGGAATC 1320

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GCTAGTAATC GTAGATCAGC CATGCTACGG TGAATACGTT CCCGGGTCTT GTACTCACCG	1380
CCCGTCACAC CATGGGAGTT GATTTCACCTC GAAGCCGGAA TACTAAACTA GTTACCGTCC	1440
ACAGTGGAAT CAGCGACTGG GGTGAAGTCG TAACAAGGTA ACCGTAGGAG AACCTGCGGT	1500
TGGATCACCT CCT	1513

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

TTTTATGGAG AGTTTGATCC TGGCTCAGGA TGAACGCTGG CGGCGTGCCT AATACATGCA	60
AGTCGAGCGA ACGGACGAGA AGCTTGCTTC TCTGATGTTA GCGGCGGACG GGTGAGTAAC	120
ACGTGGATAA CCTACCTATA AGACTGGGAT AACTTCGGGA AACCGGAGCT AATACCGGAT	180
AATATTTTGA ACCGCATGGT TCAAAAGTGA AAGACGGTCT TGCTGTCACT TATAGATGGA	240
TCCGCGCTGC ATTAGCTAGT TGGTAAGGTA ACGGCTTACC AAGGCAACGA TACGTAGCCG	300
ACCTGAGAGG GTGATCGGCC AACTTGAAC TGAGACACGG TCCAGACTCC TACGGGAGGC	360
AGCAGTAGGG AATCTTCCGC AATGGGCGAA AGCCTGACGG AGCAACGCCG CGTGAGTGAT	420
GAAGGTCTTC GGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACTGTG	480
CACATCTTGA CGGTACCTAA TCAGAAAGCC ACGGCTAACT ACGTGCCAGC AGCCGCGGTA	540
ATACGTAGGT GGCAAGCGTT ATCCGGAATT ATTGGGCGTA AAGCGCGCGT AGGCGGTTTT	600
TTAAGTCTGA TGTGAAAGCC CACGGCTCAA CCGTGGAGGG TCATTGGAAA CTGGAAAAC	660
TGAGTGCAGA AGAGGAAAGT GGAATTCCAT GTGTAGCGGT GAAATGCGCA GAGATATGGA	720
GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAACTG ACGCTGATGT GCGAAAGCGT	780
GGGGATCAAA CAGGATTAGA TACCCTGGTA GTCCACGCCG TAAACGATGA GTGCTAAGTG	840
TTAGGGGGTT TCCGCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCTGGGGAGT	900
ACGACCGCAA GGTTGAAACT CAAAGGAATT GACGGGGACC CGCACAAGCG GTGGAGCATG	960
TGGTTTAATT CGAAGCAACG CGAAGAACCT TACCAAATCT TGACATCCTT TGACAACTCT	1020
AGAGATAGAG CCTTCCCCTT CGGGGGACAA AGTGACAGGT GGTGCATGGT TGTCGTCAGC	1080
TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCTTAAG CTTAGTTGCC	1140
ATCATTAAGT TGGGCACTCT AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG	1200
ACGTCAAATC ATCATGCCCC TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA	1260

AAGGGCAGCG	AAACCGCGAG	GTCAAGCAAA	TCCCATAAAG	TTGTTCTCAG	TTCGGATTGT	1320
AGTCTGCAAC	TCGACTACAT	GAAGCTGGAA	TCGCTAGTAA	TCGTAGATCA	GCATGCTACG	1380
GTGAATACGT	TCCCGGGTAT	TGTACACACC	GCCCGTCACA	CCACGAGAGT	TTGTAACACC	1440
CGAAGCCGGT	GGAGTAACCT	TTTAGGAGCT	AGCCGTCGAA	GGTGGGACAA	ATGATTGGGG	1500
TGAAGTCGTA	ACAAGGTAGC	CGTATCGGAA	GGTGCGGCTG	GATCACCTCC	TTTCT	1555

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